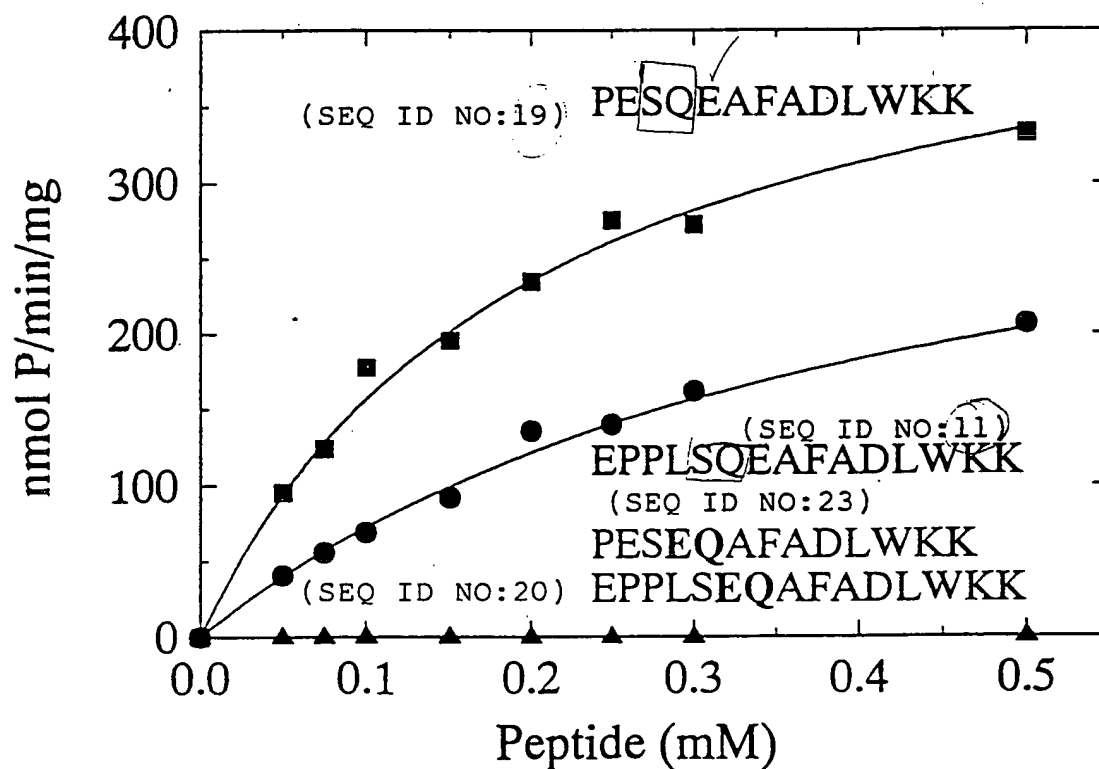


FIGURE 1

Phosphorylation of Synthetic Peptides by Human DNA-PK



004207-2E456960

FIGURE 2

Phosphorylation of Synthetic Peptides by Purified Human DNA-PK

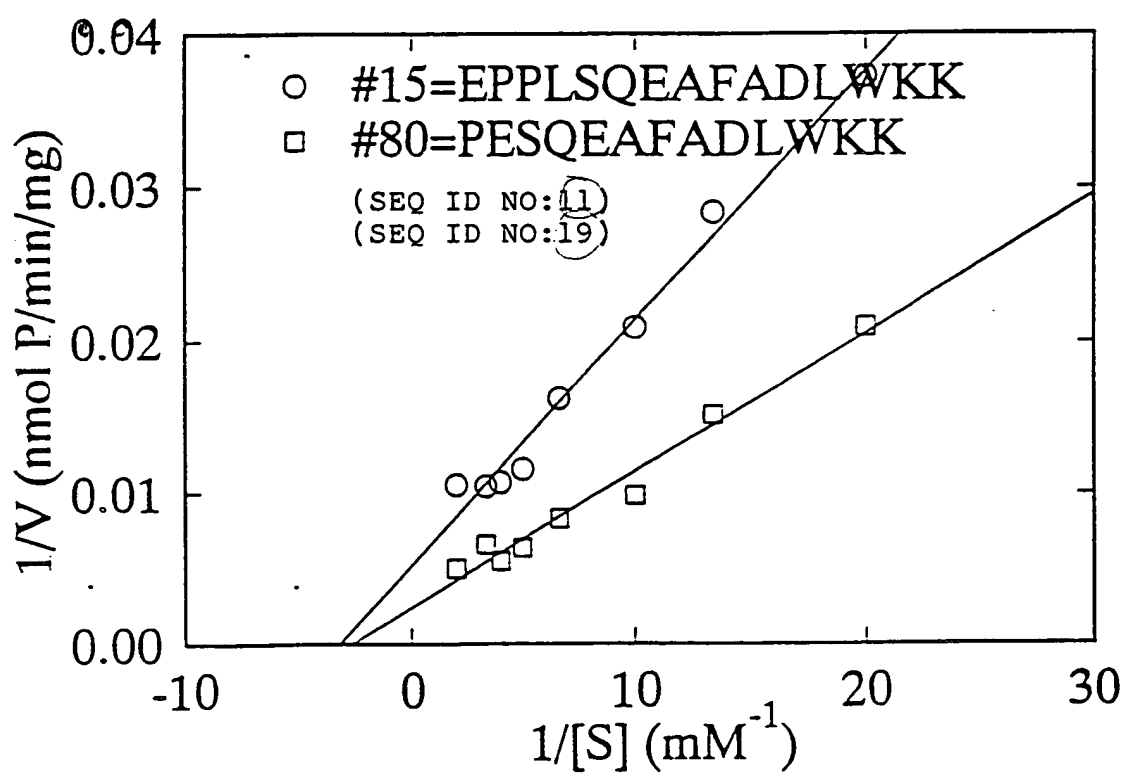
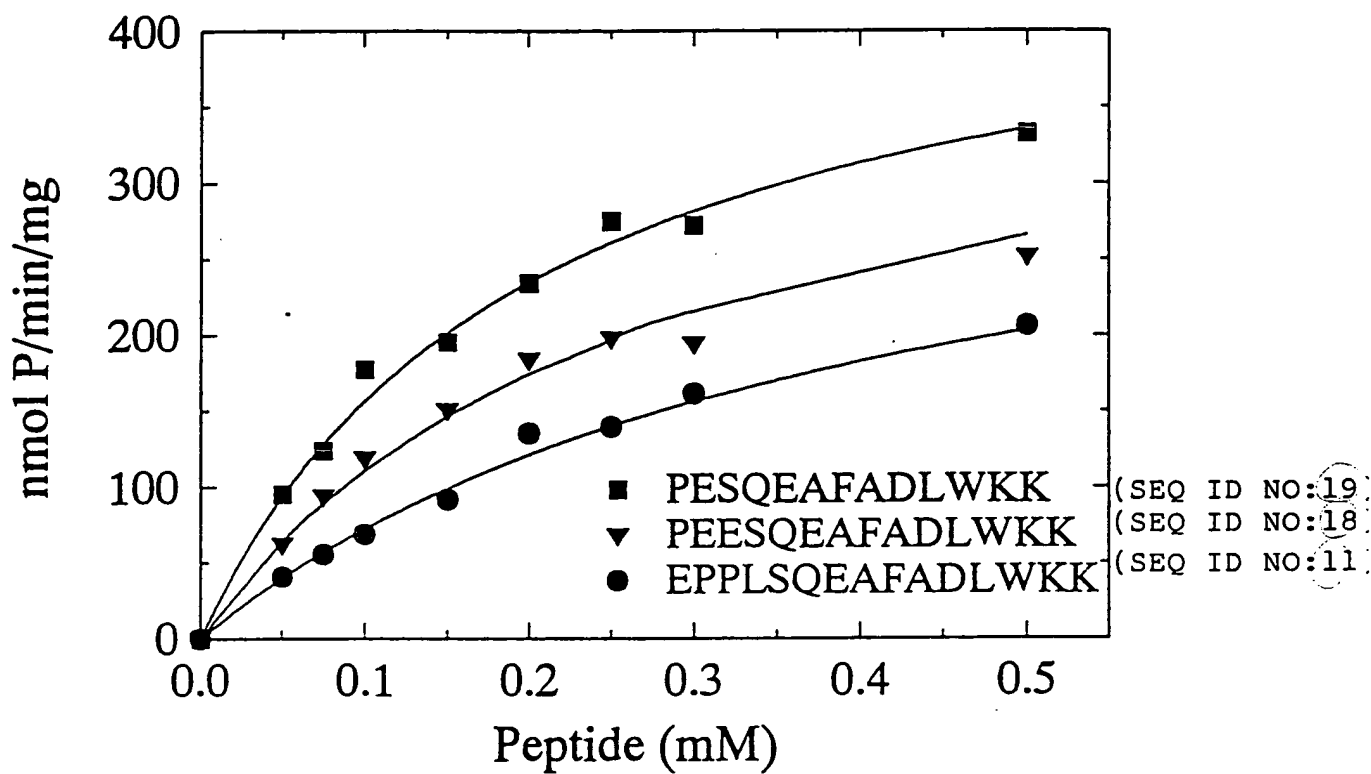


FIGURE 3

Phosphorylation of Synthetic Peptides by Human DNA-PK



Artificial DNA-PK Substrates

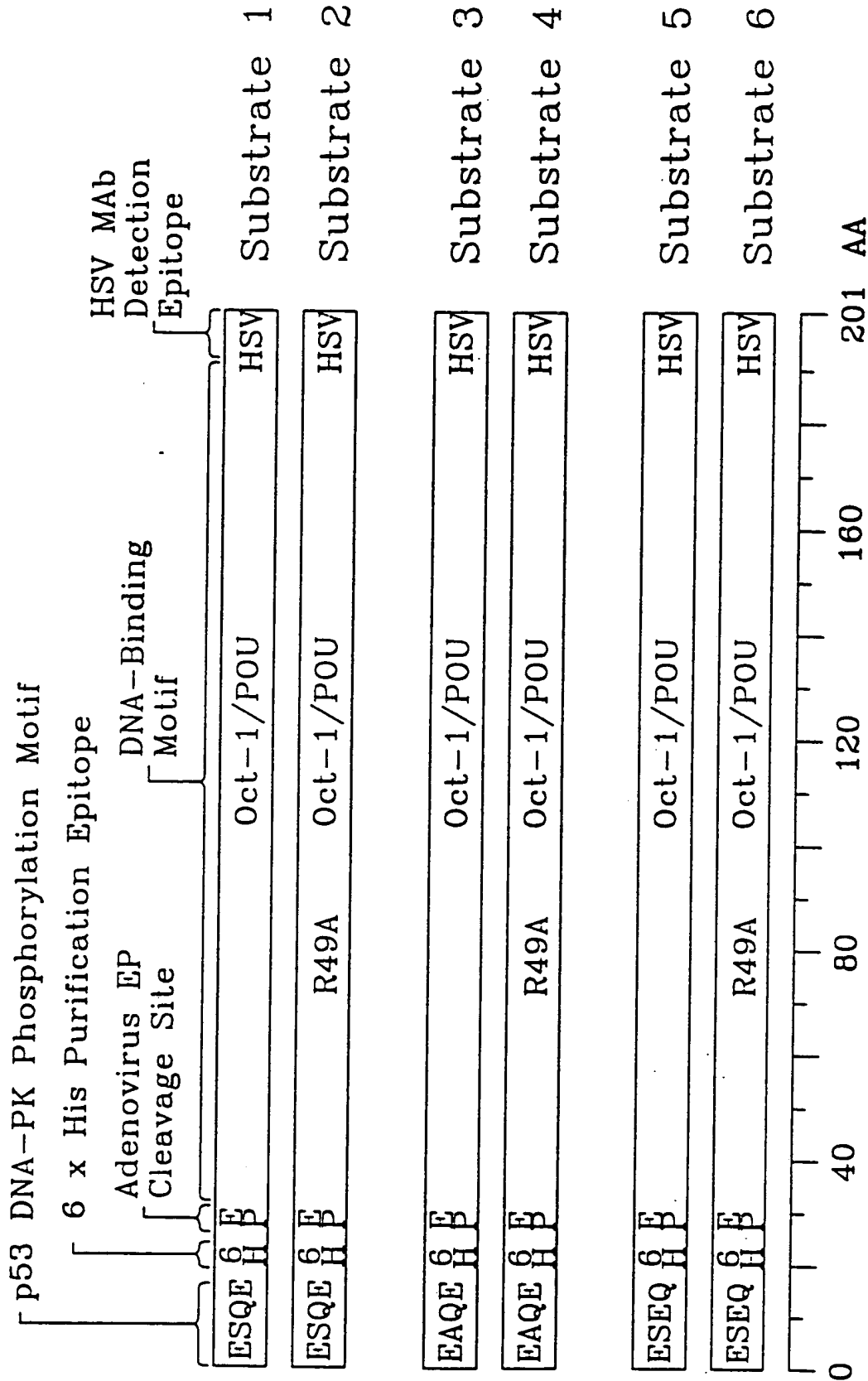


FIGURE 4

FIGURE 5A

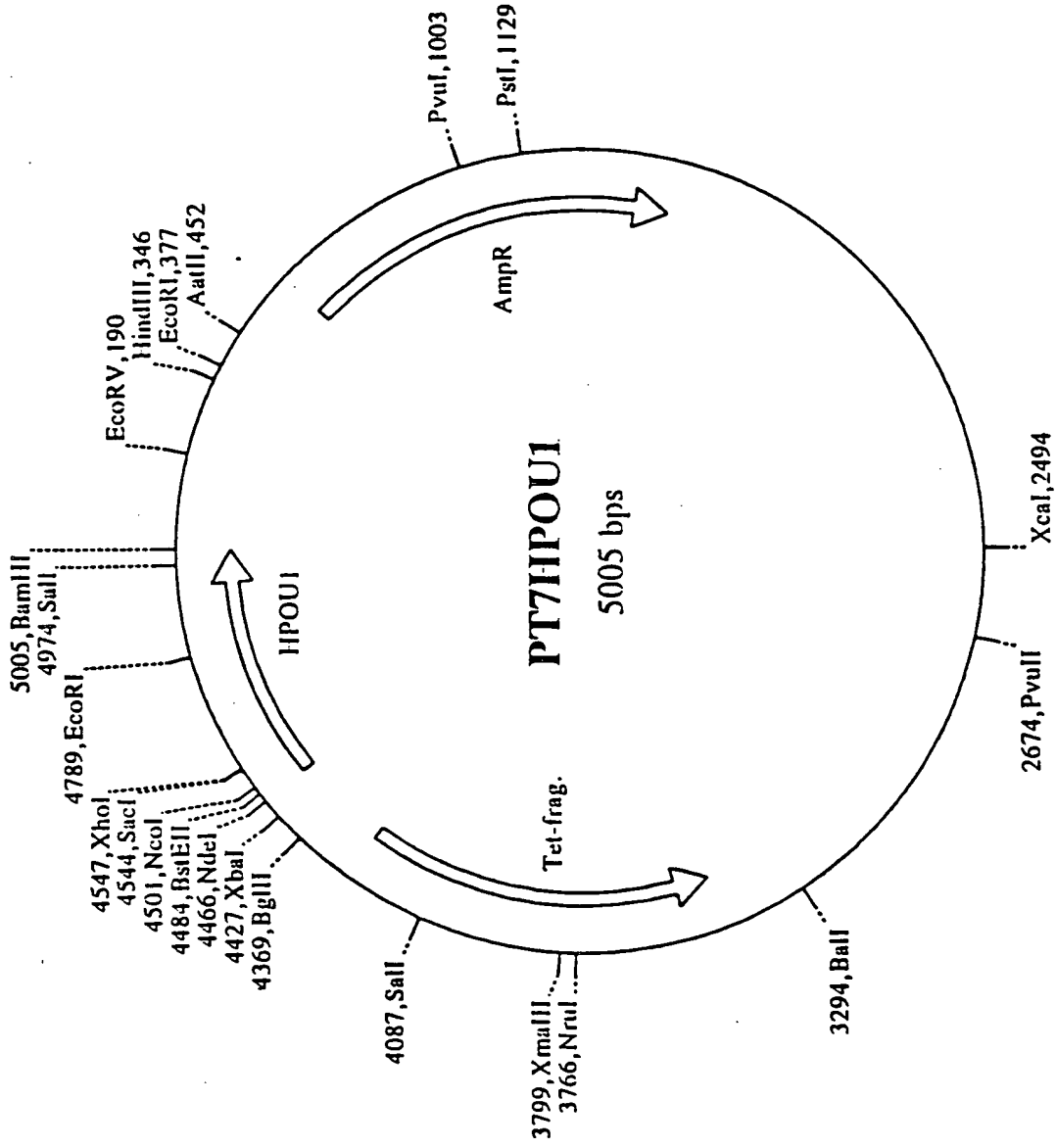


FIGURE 5B

Expressed Prot in Product of pT7HPOU1

pT7HPOU1: Expression Vector for Human Oct-1 POU Domain with His6 leader

T7HPOU1 5005 bases, circular

Lab Strain: #236 = pT7HPOU1/DH5[alpha]

Lab Strain: #237 = pT7HPOU1/BL21(DE3)

Plasmid Construction:

Vector: pT7HIS2 (pET-3 with His6 leader and T7 gene 2.5)
Cut with Nco I and BamH I

Insert: POU domain from pET11c-OCT1POU (CWA Strain #234) from Winship Herr, Cold Spring Harbor Laboratory. POU domain DNA was made by PCR using primers #761 and #430 (pBR322 EcoR I site). PCR fragment was cut with NcoI and BamHI, purified, and inserted in similarly cut pT7HIS2 vector (also called pT7AdEP-DBP).

PREDICTED PROTEIN SEQUENCE OF EXPRESSION PRODUCT

Segment: 4469-5005

(SEQ ID NO:59)

Composition

8 Ala	7 Gln	18 Leu	18 Ser
12 Arg	17 Glu	15 Lys	9 Thr
11 Asn	11 Gly	8 Met	2 Trp
6 Asp	6 His	8 Phe	1 Tyr
2 Cys	9 Ile	6 Pro	4 Val

Mol. wt. unmod. chain = 20,352

Number of residues = 178

Met Ala Ser Met Thr Gly His His His His His His Gly Met Ser Gly
1 5 10 15

Gly Met Glu Glu Pro Ser Asp Leu Glu Glu Leu Glu Gln Phe Ala Lys
20 25 30

Thr Phe Lys Gln Arg Arg Ile Lys Leu Gly Phe Thr Gln Gly Asp Val
35 40 45

Gly Leu Ala Met Gly Lys Leu Tyr Gly Asn Asp Phe Ser Gln Thr Thr
50 55 60

004037-103400

FIGURE 5B (Continued)

(SEQ ID NO:59)

Ile Ser Arg Phe Glu Ala Leu Asn Leu Ser Phe Lys Asn Met Cys Lys
65 70 75 80

Leu Lys Phe Leu Leu Glu Lys Trp Leu Asn Asp Ala Glu Asn Leu Ser
85 90 95

Ser Asp Ser Ser Leu Ser Ser Pro Ser Ala Leu Asn Ser Pro Gly Ile
100 105 110

Glu Gly Leu Ser Arg Arg Arg Lys Lys Arg Thr Ser Ile Glu Thr Asn
115 120 125

Ile Arg Val Leu Glu Lys Ser Phe Leu Glu Asn Gln Lys Pro Thr Ser
130 135 140

Glu Glu Ile Thr Met Ile Ala Asp Gln Leu Asn Met Glu Lys Glu Val
145 150 155 160

Ile Arg Val Trp Phe Cys Asn Arg Arg Gln Lys Glu Lys Arg Ile Asn
165 170 175

Pro

Reference: Anderson, C. W., and S. P. Lees-Miller. 1992. The nuclear serine/threonine protein kinase DNA-PK. Crit. Rev. Eukaryotic Gene Express. 2, 283-314.

004201-2456960

Figure 5C

NUCLEOTIDE SEQUENCE OF pT7HPOU1

(SEQ ID NO:60)

GATCCACAGG	ACGGGTGTGG	TCGCCATGAT	CGCGTAGTCG	ATAGTGGCTC	CAAGTAGCGA	60
AGCGAGCAGG	ACTGGGCGGC	GGCCAAAGCG	GTCGGACAGT	GCTCCGAGAA	CGGGTGCGCA	120
TAGAAATTGC	ATCAACGCAT	ATAGCGCTAG	CAGCACGCCA	TAGTGA CTGG	CGATGCTGTC	180
GGAATGGACG	ATATCCCGCA	AGAGGCCCGG	CAGTACCGGC	ATAACCAAGC	CTATGCCTAC	240
AGCATCCAGG	GTGACGGTGC	CGAGGATGAC	GATGAGCGCA	TTGTTAGATT	TCATACACGG	300
TGCCTGACTG	CGTTAGCAAT	TTAACTGTGA	TAAACTACCG	CATTAAAGCT	TATCGATGAT	360
AAGCTGTCAA	ACATGAGAAT	TCTTGAAGAC	GAAAGGGCCT	CGTGATACGC	CTATTTTTAT	420
AGGTTAATGT	CATGATAATA	ATGGTTTCTT	AGACGTCAGG	TGGCACTTTT	CGGGGAAATG	480
TGCGCGGAAC	CCCTATTTGT	TTATTTTTCT	AAATACATTC	AAATATGTAT	CCGCTCATGA	540
GACAATAACC	CTGATAAATG	CTTCAATAAT	ATTGAAAAAG	GAAGAGTATG	AGTATTCAAC	600
ATTTCCGTGT	CGCCCTTATT	CCCTTTTTTG	CGGCATTTTG	CCTTCCTGTT	TTTGCTCACC	660
CAGAAACGCT	GGTGAAAGTA	AAAGATGCTG	AAGATCAGTT	GGGTGCACGA	GTGGGTTACA	720
TCGAACTGGA	TCTCAACAGC	GGTAAGATCC	TTGAGAGTTT	TCGCCCCGAA	GAACGTTTTTC	780
CAATGATGAG	CACTTTTAAA	GTTCTGCTAT	GTGGCGCGGT	ATTATCCCGT	GTTGACGCCG	840
GGCAAGAGCA	ACTCGGTGCG	CGCATACACT	ATTCTCAGAA	TGACTTG GTT	GAGTACTCAC	900
CAGTCACAGA	AAAGCATCTT	ACGGATGGCA	TGACAGTAAG	AGAATTATGC	AGTGCTGCCA	960
TAACCATGAG	TGATAACACT	GCGGCCAACT	TACTTCTGAC	AACGATCGGA	GGACCGAAGG	1020
AGCTAACCGC	TTTTTTGCAC	AACATGGGGG	ATCATGTAAC	TCGCCTTGAT	CGTTGGGAAC	1080
CGGAGCTGAA	TGAAGCCATA	CCAAACGACG	AGCGTGACAC	CACGATGCCT	GCAGCAATGG	1140
CAACAACGTT	GCGCAAATA	TTAACTGGCG	AACTACTTAC	TCTAGCTTCC	CGGCAACAAT	1200
TAATAGACTG	GATGGAGGCG	GATAAAGTTG	CAGGACCACT	TCTGCGCTCG	GCCCTTCCGG	1260
CTGGCTGGTT	TATTGCTGAT	AAATCTGGAG	CCGGTGAGCG	TGGGTCTCGC	GGTATCATTG	1320
CAGCACTGGG	GCCAGATGGT	AAGCCCTCCC	GTATCGTAGT	TATCTACACG	ACGGGGAGTC	1380

Figure 5C (Continued)

(SEQ ID NO:60)

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AGGCAACTAT GGATGAACGA AATAGACAGA TCGCTGAGAT AGGTGCCTCA CTGATTAAGC 1440
ATTGGTAACT GTCAGACCAA GTTTACTCAT ATATACTTTA GATTGATTTA AAAC TTCATT 1500
TTTAATTTAA AAGGATCTAG GTGAAGATCC TTTT TGATAA TCTCATGACC AAAATCCCTT 1560
AACGTGAGTT TTCGTTCCAC TGAGCGTCAG ACCCCGTAGA AAAGATCAAA GGATCTTCTT 1620
GAGATCCTTT TTTTCTGCGC GTAATCTGCT GCTTGCAAAC AAAAAAACCA CCGCTACCAG 1680
CGGTGGTTTG TTTGCCGGAT CAAGAGCTAC CAACTCTTTT TCCGAAGGTA ACTGGCTTCA 1740
GCAGAGCGCA GATACCAAAT ACTGTCCTTC TAGTGTAGCC GTAGTTAGGC CACCACTTCA 1800
AGAACTCTGT AGCACCGCCT ACATACCTCG CTCTGCTAAT CCTGTTACCA GTGGCTGCTG 1860
CCAGTGGCGA TAAGTCGTGT CTTACCGGGT TGGACTCAAG ACGATAGTTA CCGGATAAGG 1920
CGCAGCGGTC GGGCTGAACG GGGGGTTCGT GCACACAGCC CAGCTTGGAG CGAACGACCT 1980
ACACCGAACT GAGATACCTA CAGCGTGAGC ATTGAGAAAG CGCCACGCTT CCCGAAGGGA 2040
GAAAGGCGGA CAGGTATCCG GTAAGCGGCA GGGTCGGAAC AGGAGAGCGC ACGAGGGAGC 2100
TTCCAGGGGG AAACGCCTGG TATCTTTATA GTCCTGTCGG GTTTCGCCAC CTCTGACTTG 2160
AGCGTCGATT TTTGTGATGC TCGTCAGGGG GCGGAGCCT ATGGAAAAAC GCCAGCAACG 2220
CGGCCTTTTT ACGGTTCTTG GCCTTTTGCT GGCCTTTTGC TCACATGTTC TTTCTGCGT 2280
TATCCCCTGA TTCTGTGGAT AACCGTATTA CCGCCTTTGA GTGAGCTGAT ACCGCTCGCC 2340
GCAGCCGAAC GACCGAGCGC AGCGAGTCAG TGAGCGAGGA AGCGGAAGAG CGCCTGATGC 2400
GGTATTTTCT CCTTACGCAT CTGTGCGGTA TTTCACACCG CATATATGGT GCACTCTCAG 2460
TACAATCTGC TCTGATGCCG CATAGTTAAG CCAGTATACA CTCCGCTATC GCTACGTGAC 2520
TGGGTCATGG CTGCGCCCCG ACACCCGCCA ACACCCGCTG ACGCGCCCTG ACGGGCTTGT 2580
CTGCTCCCGG CATCCGCTTA CAGACAAGCT GTGACCGTCT CCGGGAGCTG CATGTGTCAG 2640
AGGTTTTTAC CGTCATCACC GAAACGCGCG AGGCAGCTGC GGTAAGCTC ATCAGCGTGG 2700
TCGTGAAGCG ATTCACAGAT GTCTGCCTGT TCATCCGCGT CCAGCTCGTT GAGTTTCTCC 2760

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Figure 5C (Continued)

(SEQ ID NO:60)

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AGAAGCGTTA ATGTCTGGCT TCTGATAAAG CGGGCCATGT TAAGGGCGGT TTTTTCCTGT 2820
TTGGTCACTG ATGCCTCCGT GTAAGGGGGA TTTCTGTTCA TGGGGGTAAT GATACCGATG 2880
AAACGAGAGA GGATGCTCAC GATACGGGTT ACTGATGATG AACATGCCCC GTTACTGGAA 2940
CGTTGTGAGG GTAAACAACT GGCGGTATGG ATGCGGCGGG ACCAGAGAAA AATCACTCAG 3000
GGTCAATGCC AGCGCTTCGT TAATACAGAT GTAGGTGTTT CACAGGGTAG CCAGCAGCAT 3060
CCTGCGATGC AGATCCGGAA CATAATGGTG CAGGGCGCTG ACTTCCGCGT TTCCAGACTT 3120
TACGAAACAC GGAAACCGAA GACCATTTCAT GTTGTTGCTC AGGTCGCAGA CGTTTTGCAG 3180
CAGCAGTCGC TTCACGTTCG CTCGCGTATC GGTGATTTCAT TCTGCTAACC AGTAAGGCAA 3240
CCCCGCCAGC CTAGCCGGGT CCTCAACGAC AGGAGCACGA TCATGCGCAC CCGTGGCCAG 3300
GACCCAACGC TGCCCGAGAT GCGCCGCGTG CGGCTGCTGG AGATGGCGGA CGCGATGGAT 3360
ATGTTCTGCC AAGGGTTGGT TTGCGCATTC ACAGTTCTCC GCAAGAATTG ATTGGCTCCA 3420
ATTCTTGAG TGGTGAATCC GTTAGCGAGG TGCCGCCGGC TTCCATTCAG GTCGAGGTGG 3480
CCCGGCTCCA TGCACCGCGA CGCAACGCGG GGAGGCAGAC AAGGTATAGG GCGGCGCCTA 3540
CAATCCATGC CAACCCGTTT CATGTGCTCG CCGAGGCGGC ATAAATCGCC GTGACGATCA 3600
GCGGTCCAGT GATCGAAGTT AGGCTGGTAA GAGCCGCGAG CGATCCTTGA AGCTGTCCCT 3660
GATGGTCGTC ATCTACCTGC CTGGACAGCA TGGCCTGCAA CGCGGGCATC CCGATGCCGC 3720
CGGAAGCGAG AAGAATCATA ATGGGGAAGG CCATCCAGCC TCGCGTCGCG AACGCCAGCA 3780
AGACGTAGCC CAGCGCGTCG GCCGCCATGC CGGCGATAAT GGCCTGCTTC TCGCCGAAAC 3840
GTTTGGTGGC GGGACCAAGT ACGAAGGCTT GAGCGAGGGC GTGCAAGATT CCGAATACCG 3900
CAAGCGACAG GCCGATCATC GTCGCGCTCC AGCGAAAGCG GTCCTCGCCG AAAATGACCC 3960
AGAGCGCTGC CGGCACCTGT CCTACGAGTT GCATGATAAA GAAGACAGTC ATAAGTGCGG 4020
CGACGATAGT CATGCCCCGC GCCCACCGBA AGGAGCTGAC TGGGTTGAAG GCTCTCAAGG 4080
GCATCGGTGC ACGCTCTCCC TTATGCGACT CCTGCATTAG GAAGCAGCCC AGTAGTAGGT 4140

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Figure 5C (Continued)

(SEQ ID NO:60)

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TGAGGCCGTT GAGCACCGCC GCCGCAAGGA ATGGTGCATG CAAGGAGATG GCGCCCAACA 4200
GTCCCCCGGC CACGGGGCCT GCCACCATAC CCACGCCGAA ACAAGCGCTC ATGAGCCCGA 4260
AGTGGCGAGC CCGATCTTCC CCATCGGTGA TGTCGGCGAT ATAGGCGCCA GCAACCGCAC 4320
CTGTGGCGCC GGTGATGCCG GCCACGATGC GTCCGGCGTA GAGGATCGAG ATCTCGATCC 4380
CGCGAAATTA ATACGACTCA CTATAGGGAG ACCACAACGG TTTCCCTCTA GAAATAATTT 4440
TGTTTAACTT TAAGAAGGAG ATATACAT ATG GCT TCT ATG ACT GGT CAC CAC 4492
CAC CAT CAC CAT GGT ATG AGC GGC GGC ATG GAG GAG CCC AGT GAC CTT 4540
GAG GAG CTC GAG CAG TTT GCC AAG ACC TTC AAA CAA AGA CGA ATC AAA 4588
CTT GGA TTC ACT CAG GGT GAT GTT GGG CTC GCT ATG GGG AAA CTA TAT 4636
GGA AAT GAC TTC AGC CAA ACT ACC ATC TCT CGA TTT GAA GCC TTG AAC 4684
CTC AGC TTT AAG AAC ATG TGC AAG TTG AAG CCA CTT TTA GAG AAG TGG 4732
CTA AAT GAT GCA GAG AAC CTC TCA TCT GAT TCG TCC CTC TCC AGC CCA 4780
AGT GCC CTG AAT TCT CCA GGA ATT GAG GGC TTG AGC AGG CGC AGG AAG 4828
AAA CGC ACC AGC ATA GAG ACC AAC ATC CGT GTG GCC TTA GAG AAG AGT 4876
TTC TTG GAG AAT CAA AAG CCT ACC TCG GAA GAG ATC ACT ATG ATT GCT 4924
GAT CAG CTC AAT ATG GAA AAA GAG GTG ATT CGT GTT TGG TTC TGT AAC 4972
CGT CGA CAG AAA GAA AAA AGA ATC AAC CCA TAG 5005

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FIGURE 6

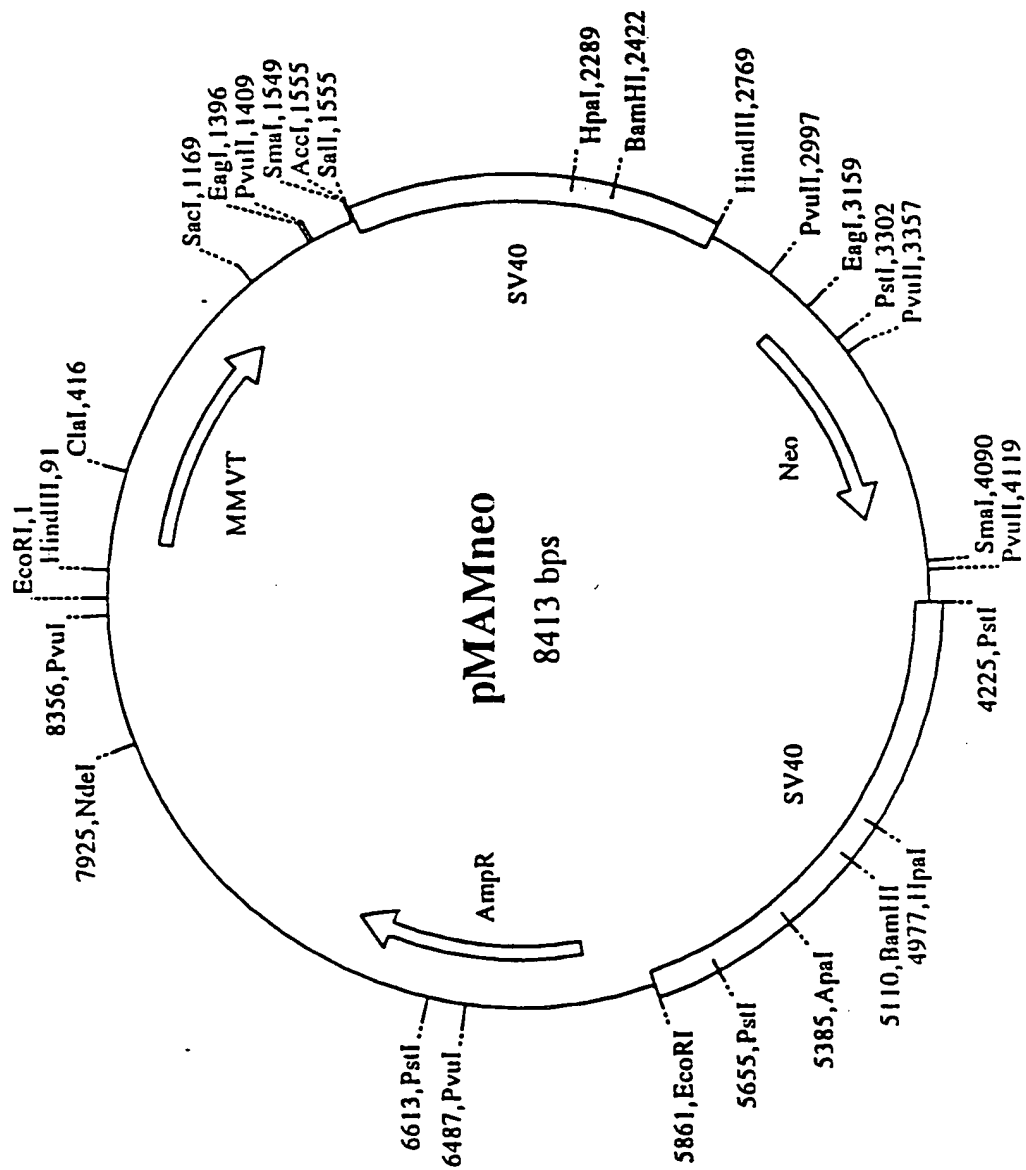


FIGURE 6A

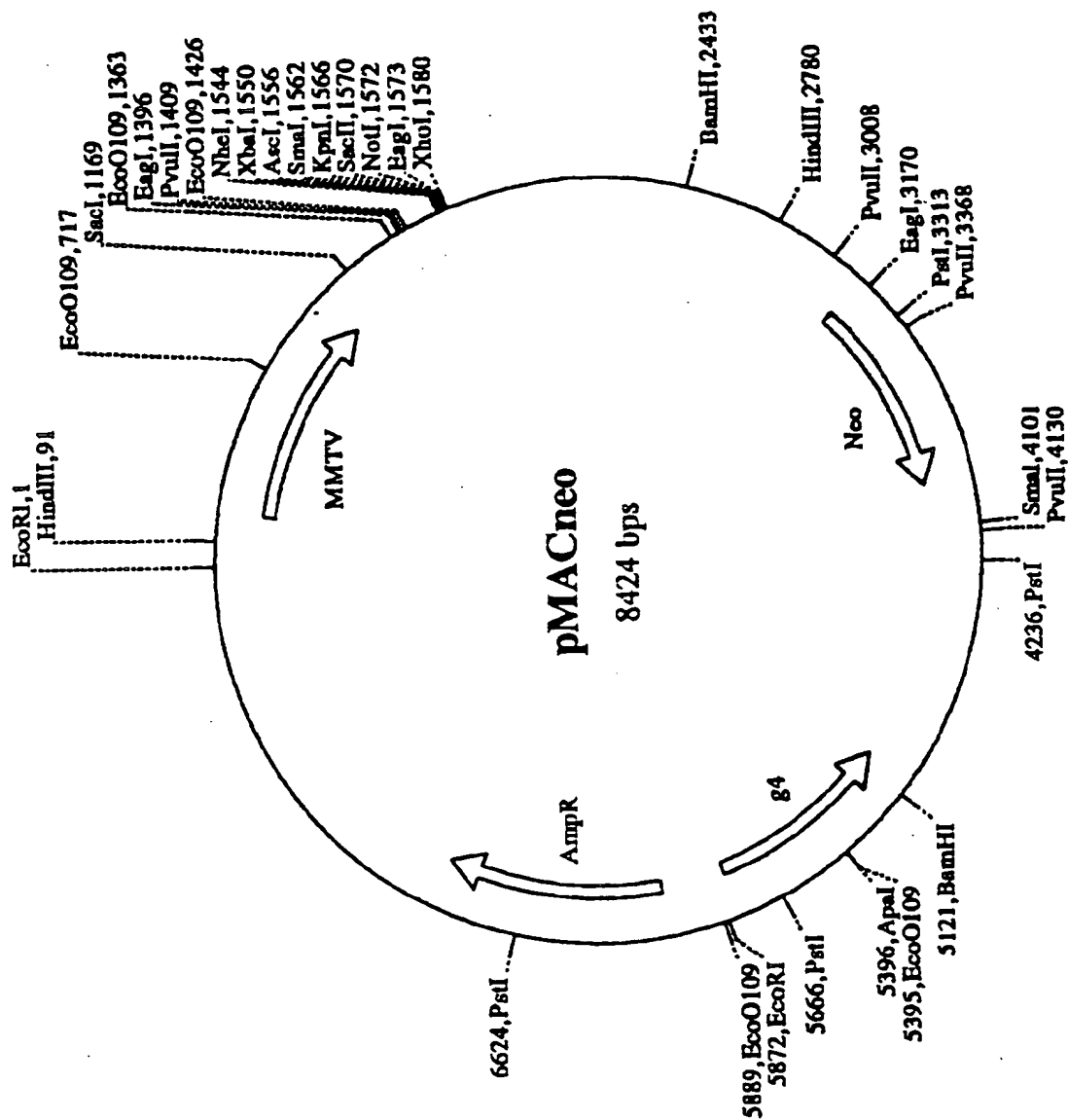


FIGURE 7

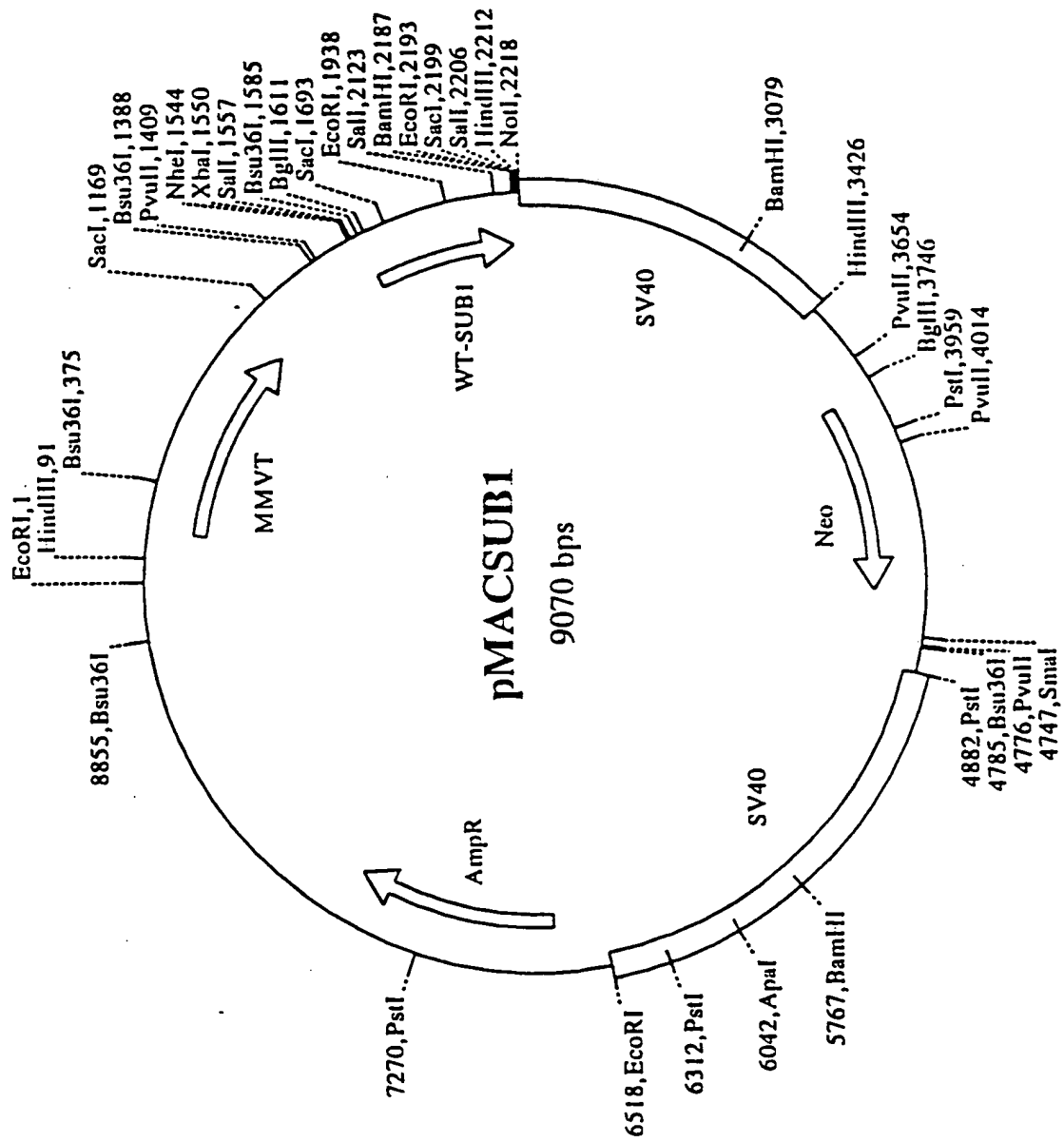


FIGURE 8A

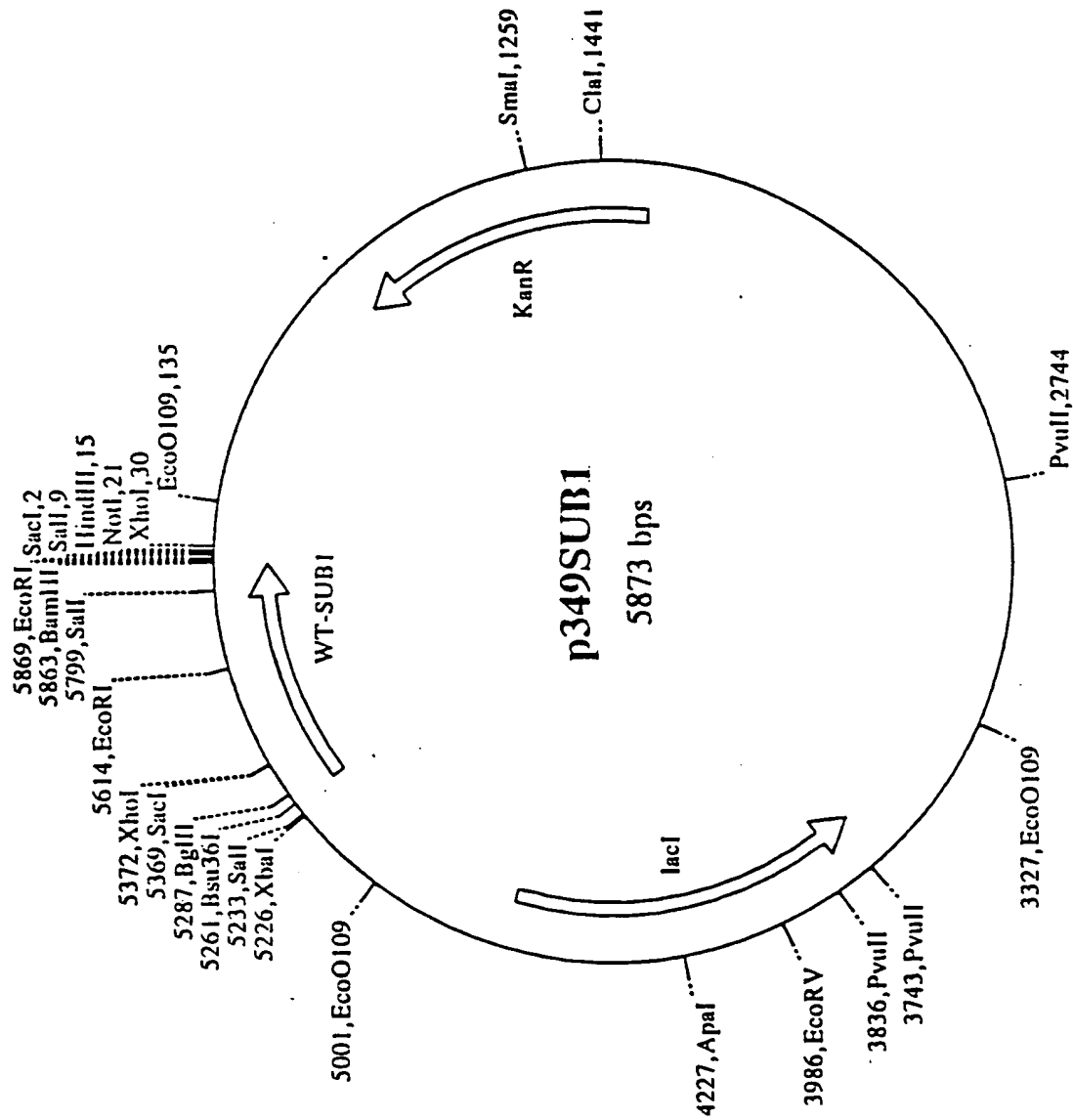


FIGURE 8B

Wild-Type Artificial DNA-PK Substrat 1

Lab Stain: #349 = p349SUB1 in DH5[alpha]
 Lab Strain #351 = p349SUB1 in BL21(DE3)

Plasmid Construction:

VECTOR: p410 = derivative pET-28a (Novagen) without BglIII site
 INSERT: Substrate encoding XbaI-BamHI fragment was excised from
 p345 with XbaI and BamHI and cloned into XbaI and BamHI
 cleaved p410.

ANTIBIOTIC SELECTION: 50 ug/ml Kanamycin

PREDICTED SEQUENCE POUSUB1 ARTIFICIAL DNA-PK SUBSTRATE

Segment: 5258-5860

(SEQ ID NO: 61)

Composition

8 Ala	9 Gln	22 Leu	18 Ser
12 Arg	24 Glu	16 Lys	9 Thr
11 Asn	11 Gly	7 Met	3 Trp
9 Asp	6 His	9 Phe	1 Tyr
2 Cys	9 Ile	11 Pro	4 Val

Mol. wt. unmod. chain = 23,126

Number of residues = 201

Met Pro Glu Glu Ser Gln Glu Thr Phe Glu Asp Leu Trp Lys Leu Leu
 1 5 10 15

Pro Gly His His His His His His Gly Met Ser Gly Gly Met Glu Glu
 20 25 30

Pro Ser Asp Leu Glu Glu Leu Glu Gln Phe Ala Lys Thr Phe Lys Gln
 35 40 45

Arg Arg Ile Lys Leu Gly Phe Thr Gln Gly Asp Val Gly Leu Ala Met
 50 55 60

Gly Lys Leu Tyr Gly Asn Asp Phe Ser Gln Thr Thr Ile Ser Arg Phe
 65 70 75 80

Glu Ala Leu Asn Leu Ser Phe Lys Asn Met Cys Lys Leu Lys Pro Leu
 85 90 95

Leu Glu Lys Trp Leu Asn Asp Ala Glu Asn Leu Ser Ser Asp Ser Ser
 100 105 110

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FIGURE 8B (Continued)

(SEQ ID NO:61)

Leu Ser Ser Pro Ser Ala Leu Asn Ser Pro Gly Ile Glu Gly Leu Ser
115 120 125

Arg Arg Arg Lys Lys Arg Thr Ser Ile Glu Thr Asn Ile Arg Val Ala
130 135 140

Leu Glu Lys Ser Phe Leu Glu Asn Gln Lys Pro Thr Ser Glu Glu Ile
145 150 155 160

Thr Met Ile Ala Asp Gln Leu Asn Met Glu Lys Glu Val Ile Arg Val
165 170 175

Trp Phe Cys Asn Arg Arg Gln Lys Glu Lys Arg Ile Asn Pro Gln Pro
180 185 190

Glu Leu Ala Pro Glu Asp Pro Glu Asp
195 200

NOTES:

- Ser 5-Gln 6 = Artificial DNA-PK Site
- Glu 10 = Introduced to make BglII site, =Ser in p53,
=Ala in peptide
- His 19-His 24 = His tag for Zn/Ni-affinity chromatography
- Met 26-Gly 29 = Adenovirus Proteinase Cleavage Motif
- Glu 31-Pro 190 = POU specific domain of Human Oct-1
- Gln 191-Asp 201 = Novagen HSV Epitope Tag

004207-2E156950

Figure 8C

NUCLEOTIDE SEQUENCE OF p349SUB1

(SEQ ID NO:62)

CGAGCTCCGT	CGACAAGCTT	GCGGCCGCAC	TCGAGCACCA	CCACCACCAC	CACTGAGATC	60
CGGCTGCTAA	CAAAGCCCGA	AAGGAAGCTG	AGTTGGCTGC	TGCCACCGCT	GAGCAATAAC	120
TAGCATAACC	CCTTGGGGCC	TCTAAACGGG	TCTTGAGGGG	TTTTTTGCTG	AAAGGAGGAA	180
CTATATCCGG	ATTGGCGAAT	GGGACGCGCC	CTGTAGCGGC	GCATTAAGCG	CGGCGGGTGT	240
GGTGGTTACG	CGCAGCGTGA	CCGCTACACT	TGCCAGCGCC	CTAGCGCCCG	CTCCTTTCGC	300
TTTCTTCCCT	TCCTTTCTCG	CCACGTTTCG	CGGCTTTCCC	CGTCAAGCTC	TAAATCGGGG	360
GCTCCCTTTA	GGGTTCGAT	TTAGTGCTTT	ACGGCACCTC	GACCCCAAAA	AACTTGATTA	420
GGGTGATGGT	TCACGTAGTG	GGCCATCGCC	CTGATAGACG	GTTTTTCGCC	CTTTGACGTT	480
GGAGTCCACG	TTCTTTAATA	GTGGACTCTT	GTTCCAAACT	GGAACAACAC	TCAACCCTAT	540
CTCGGTCTAT	TCTTTTGATT	TATAAGGGAT	TTTGCCGATT	TCGGCCTATT	GGTTAAAAAA	600
TGAGCTGATT	TAACAAAAAT	TTAACGCGAA	TTTTAACAAA	ATATTAACGT	TTACAATTTT	660
AGGTGGCACT	TTTCGGGGAA	ATGTGCGCGG	AACCCCTATT	TGTTTATTTT	TCTAAATACA	720
TTCAAATATG	TATCCGCTCA	TGAATTAATT	CTTAGAAAAA	CTCATCGAGC	ATCAAATGAA	780
ACTGCAATTT	ATTCATATCA	GGATTATCAA	TACCATATTT	TTGAAAAAGC	CGTTTCTGTA	840
ATGAAGGAGA	AAACTCACCG	AGGCAGTTCC	ATAGGATGGC	AAGATCCTGG	TATCGGTCTG	900
CGATTCCGAC	TCGTCCAACA	TCAATACAAC	CTATTAATTT	CCCCTCGTCA	AAAATAAGGT	960
TATCAAGTGA	GAAATCACCA	TGAGTGACGA	CTGAATCCGG	TGAGAATGGC	AAAAGTTTAT	1020
GCATTTCTTT	CCAGACTTGT	TCAACAGGCC	AGCCATTACG	CTCGTCATCA	AAATCACTCG	1080
CATCAACCAA	ACCGTTATTC	ATTCGTGATT	GCGCCTGAGC	GAGACGAAAT	ACGCGATCGC	1140
TGTTAAAAGG	ACAATTACAA	ACAGGAATCG	AATGCAACCG	GCGCAGGAAC	ACTGCCAGCG	1200
CATCAACAAT	ATTTTCACCT	GAATCAGGAT	ATTCTTCTAA	TACCTGGAAT	GCTGTTTTTC	1260
CGGGGATCGC	AGTGGTGAGT	AACCATGCAT	CATCAGGAGT	ACGGATAAAA	TGCTTGATGG	1320
TCGGAAGAGG	CATAAATTCC	GTCAGCCAGT	TTAGTCTGAC	CATCTCATCT	GTAACATCAT	1380

Figure 8C (Continued)

(SEQ ID NO:62)

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TGGCAACGCT ACCTTTGCCA TGTTTCAGAA ACAACTCTGG CGCATCGGGC TTCCCATACA 1440
ATCGATAGAT TGTCGCACCT GATTGCCCGA CATTATCGCG AGCCCATTTA TACCCATATA 1500
AATCAGCATC CATGTTGGAA TTTAATCGCG GCCTAGAGCA AGACGTTTCC CGTTGAATAT 1560
GGCTCATAAC ACCCCTTGTA TTA CTGTTTA TGTAAGCAGA CAGTTTTTATT GTTCATGACC 1620
AAAATCCCTT AACGTGAGTT TTCGTTCCAC TGAGCGTCAG ACCCCGTTAG AAAGATCAAA 1680
GGATCTTCTT GAGATCCTTT TTTTCTGCGC GTAATCTGCT GCTTGCAAAC AAAAAACCA 1740
CCGCTACCAG CGGTGGTTTG TTTGCCGGAT CAAGAGCTAC CAACTCTTTT TCCGAAGGTA 1800
ACTGGCTTCA GCAGAGCGCA GATACCAAAT ACTGTCCTTC TAGTG TAGCC GTAGTTAGGC 1860
CACCACTTCA AGAACTCTGT AGCACC GCCT ACATACCTCG CTCTGCTAAT CCTGTTACCA 1920
GTGGCTGCTG CCAGTGGCGA TAAGTCGTGT CTTACCGGGT TGGACTCAAG ACGATAGTTA 1980
CCGATAAGG CGCAGCGGTC GGGCTGAACG GGGGGTTCGT GCACACAGCC CAGCTTGGAG 2040
CGAACGACCT ACACCGAACT GAGATACCTA CAGCGTGAGC TATGAGAAAG CGCCACGCTT 2100
CCCGAAGGGA GAAAGGCGGA CAGGTATCCG GTAAGCGGCA GGGTCGGAAC AGGAGAGCGC 2160
ACGAGGGAGC TTCCAGGGGG AAACGCCTGG TATCTTTATA GTCCTGTCCG GTTTCGCCAC 2220
CTCTGACTTG AGCGTCGATT TTTGTGATGC TCGTCAGGGG GCGGAGCCT ATGGAAAAAC 2280
GCCAGCAACG CGGCCTTTTT ACGGTTCTCT GCCTTTTGCT GGCCTTTTG CACATGTTC 2340
TTTCCTGCGT TATCCCCTGA TTCTGTGGAT AACCGTATTA CCGCCTTTGA GTGAGCTGAT 2400
ACCGCTCGCC GCAGCCGAAC GACCGAGCGC AGCGAGTCAG TGAGCGAGGA AGCGGAAGAG 2460
CGCCTGATGC GGTATTTTCT CCTTACGCAT CTGTGCGGTA TTTCACACCG CATATATGGT 2520
GCACTCTCAG TACAATCTGC TCTGATGCCG CATAGTTAAG CCAGTATACA CTCCGCTATC 2580
GCTACGTGAC TGGGTCATGG CTGCGCCCCG ACACCCGCCA ACACCCGCTG ACGCGCCCTG 2640
ACGGGCTTGT CTGCTCCCGG CATCCGCTTA CAGACAAGCT GTGACCGTCT CCGGGAGCTG 2700
CATGTGTCAG AGGTTTTTAC CGTCATCACC GAAACGCGCG AGGCAGCTGC GGTAAGCTC 2760

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Figure 8C (Continued)

(SEQ ID NO:62)

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ATCAGCGTGG TCGTGAAGCG ATTCACAGAT GTCTGCCTGT TCATCCGCGT CCAGCTCGTT 2820
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TTTTTCCTGT TTGGTCACTG ATGCCTCCGT GTAAGGGGGA TTTCTGTTCA TGGGGGTAAT 2940
GATACCGATG AAACGAGAGA GGATGCTCAC GATACGGGTT ACTGATGATG AACATGCCCCG 3000
GTTACTGGAA CGTTGTGAGG GTAAACAAC T GCGGTATGG ATGCGGCGGG ACCAGAGAAA 3060
AATCACTCAG GGTCAATGCC AGCGCTTCGT TAATACAGAT GTAGGTGTTT CACAGGGTAG 3120
CCAGCAGCAT CCTGCGATGC AGATCCGGAA CATAATGGTG CAGGGCGCTG ACTTCCGCGT 3180
TTCCAGACTT TACGAAACAC GGAAACCGAA GACCATTTCAT GTTGTTGCTC AGGTCGCAGA 3240
CGTTTTGCAG CAGCAGTCGC TTCACGTTTC CTCGCGTATC GGTGATTTCAT TCTGCTAACC 3300
AGTAAGGCAA CCCC GCCAGC CTAGCCGGGT CCTCAACGAC AGGAGCACGA TCATGCGCAC 3360
CCGTGGGGCC GCCATGCCGG CGATAATGGC CTGCTTCTCG CCGAAACGTT TGGTGGCGGG 3420
ACCAGTGACG AAGGCTTGAG CGAGGGCGTG CAAGATTCCG AATACCGCAA GCGACAGGCC 3480
GATCATCGTC GCGCTCCAGC GAAAGCGGTC CTCGCCGAAA ATGACCCAGA GCGCTGCCGG 3540
CACCTGTCCT ACGAGTTGCA TGATAAAGAA GACAGTCATA AGTGCGGCGA CGATAGTCAT 3600
GCCCCGCGCC CACCGGAAGG AGCTGACTGG GTTGAAGGCT CTCAAGGGCA TCGGTCGAGA 3660
TCCCGGTGCC TAATGAGTGA GCTAACTTAC ATTAATTGCG TTGCGCTCAC TGCCCGCTTT 3720
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CGGTTTGCGT ATTGGGCGCC AGGGTGGTTT TTCTTTTTCAC CAGTGAGACG GGCAACAGCT 3840
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CCAGCAGGCG AAAATCCTGT TTGATGGTGG TTAACGGCGG GATATAACAT GAGCTGTCTT 3960
CGGTATCGTC GTATCCCACT ACCGAGATAT CCGCACCAAC GCGCAGCCCG GACTCGGTAA 4020
TGGCGCGCAT TGC GCCAGC GCCATCTGAT CGTTGGCAAC CAGCATCGCA GTGGGAACGA 4080
TGCCCTCATT CAGCATTTGC ATGGTTTGTT GAAAACCGGA CATGGCACTC CAGTCGCCTT 4140

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Figure 8C (Continued)

(SEQ ID NO:62)

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CCCGTTCCGC TATCGGCTGA ATTTGATTGC GAGTGAGATA TTTATGCCAG CCAGCCAGAC 4200
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ATGCGACCAG ATGCTCCACG CCCAGTCGCG TACCGTCTTC ATGGGAGAAA ATAATACTGT 4320
TGATGGGTGT CTGGTCAGAG ACATCAAGAA ATAACGCCGG AACATTAGTG CAGGCAGCTT 4380
CCACAGCAAT GGCATCCTGG TCATCCAGCG GATAGTTAAT GATCAGCCCA CTGACGCGTT 4440
GCGCGAGAAG ATTGTGCACC GCCGCTTTAC AGGCTTCGAC GCCGCTTCGT TCTACCATCG 4500
ACACCACCAC GCTGGCACCC AGTTGATCGG CGCGAGATTT AATCGCCGCG ACAATTTGCG 4560
ACGGCGCGTG CAGGGCCAGA CTGGAGGTGG CAACGCCAAT CAGCAACGAC TGTTTGCCCCG 4620
CCAGTTGTTG TGCCACGCGG TTGGGAATGT AATTCAGCTC CGCCATCGCC GCTTCCACTT 4680
TTTCCCGCGT TTTCGCAGAA ACGTGGCTGG CCTGGTTCAC CACGCGGGAA ACGGTCTGAT 4740
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TGAATTGACT CTCTTCCGGG CGCTATCATG CCATACCGCG AAAGGTTTTG CGCCATTCTGA 4860
TGGTGTCCGG GATCTCGACG CTCTCCCTTA TGCGACTCCT GCATTAGGAA GCAGCCCAGT 4920
AGTAGGTTGA GGCCGTTGAG CACCGCCGCC GCAAGGAATG GTGCATGCAA GGAGATGGCG 4980
CCCAACAGTC CCCCGGCCAC GGGGCCTGCC ACCATACCCA CGCCGAAACA AGCGCTCATG 5040
AGCCCGAAGT GGCAGAGCCG ATCTTCCCA TCGGTGATGT CGGCGATATA GGCGCCAGCA 5100
ACCGCACCTG TGGCGCCGGT GATGCCGGCC ACGATGCGTC CGGCGTAGAG GATCGAGATC 5160
GATCTCGATC CCGCGAAATT AATACGACTC ACTATAGGGG AATTGTGAGC GGATAACAAT 5220
TCCCCTCTAG AAGTCGACTT TAAGAAGGAG TACCAAG ATG CCT GAG GAA AGT CAG 5275
GAG ACA TTC GAA GAT CTA TGG AAA CTA CTT CCT GGT CAC CAC CAC CAT 5323
CAC CAT GGT ATG AGC GGC GGC ATG GAG GAG CCC AGT GAC CTT GAG GAG 5371
CTC GAG CAG TTT GCC AAG ACC TTC AAA CAA AGA CGA ATC AAA CTT GGA 5419
TTC ACT CAG GGT GAT GTT GGG CTC GCT ATG GGG AAA CTA TAT GGA AAT 5467

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004207-245650

Figure 8C (Continued)

(SEQ ID NO:62)

GAC TTC AGC CAA ACT ACC ATC TCT CGA TTT GAA GCC TTG AAC CTC AGC	5515
TTT AAG AAC ATG TGC AAG TTG AAG CCA CTT TTA GAG AAG TGG CTA AAT	5563
GAT GCA GAG AAC CTC TCA TCT GAT TCG TCC CTC TCC AGC CCA AGT GCC	5611
CTG AAT TCT CCA GGA ATT GAG GGC TTG AGC AGG CGC CGT AAG AAA CGC	5659
ACC AGC ATA GAG ACC AAC ATC CGT GTG GCC TTA GAG AAG AGT TTC TTG	5707
GAG AAT CAA AAG CCT ACC TCG GAA GAG ATC ACT ATG ATT GCT GAT CAG	5755
CTC AAT ATG GAA AAA GAG GTG ATT CGT GTT TGG TTC TGT AAC CGT CGA	5803
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CCC GAG GAT TAGGATCCGA ATT	5873

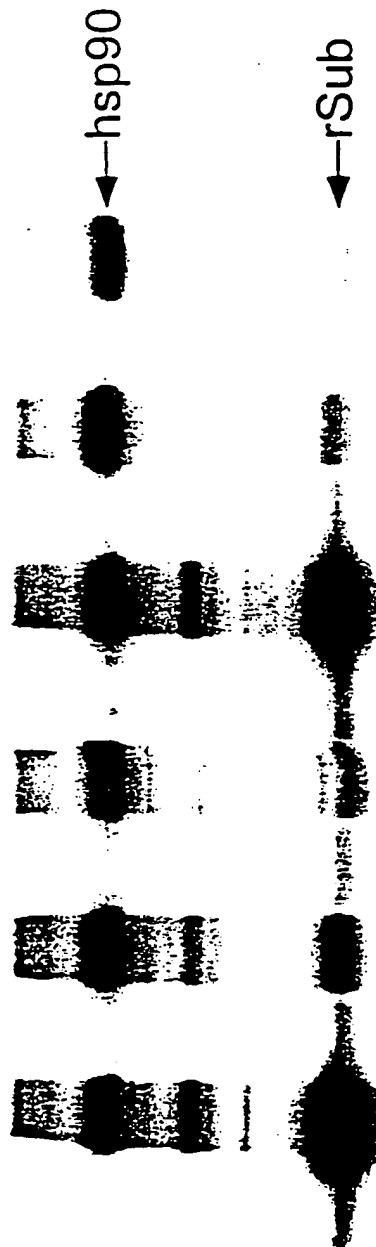
004207-2E456960

Phosphorylation of Recombinant Substrates by

Purified Human DNA-PK

1	2	3	4	5	6	Site
ESQE	EAQE	ESEQ	ESQE	EAQE	ESEQ	rSubstrate
DBP+	DBP+	DBP+	DBP-	DBP-	DBP-	CT-DNA
-	+	-	+	-	+	

Phosphoimage



Stain

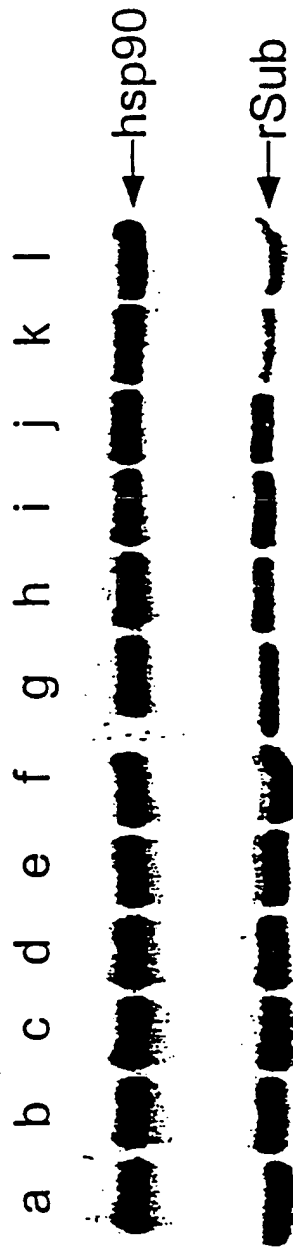


FIGURE 9

FIGURE 10

Isoelectrofocusing Analysis of Recombinant DNA-PK Substrates

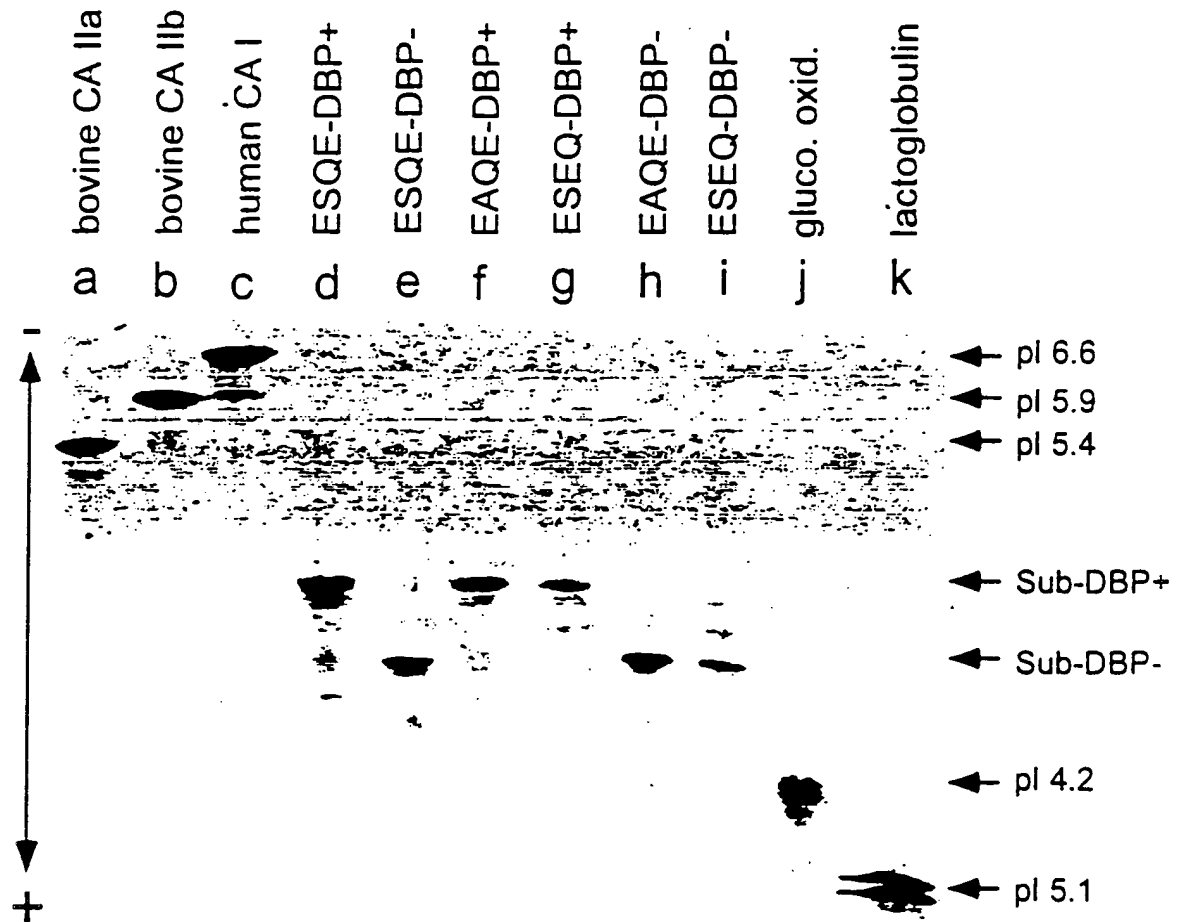


FIGURE 11

